

WHAT IS CLAIMED IS:

1. A process for the sequence analysis of polypeptides which comprise the steps of:
 - (a) degrading the polypeptide to form a mixture of polypeptide fragments which differ from each other by the presence of a terminal amino acid residue;
 - (b) analyzing the mixture in a mass spectrometer to produce data indicative of the molecular masses of each of the polypeptide fragments and;
 - (c) subtracting the molecular masses of the polypeptide fragments from each other to obtain the identification and location of the amino acid residues of the polypeptide.
2. A pre-existing mixture of sequencing-defining polypeptide chain segments, suitable for mass spectrometric readout.
3. A method of generating an amino acid sequence-defining collection of all possible length peptides (suitable for mass spectrometric readout) derived from a single polypeptide chain using *in vitro* translation of the corresponding in RNA.

cf. § 3 (STANDARD METHOD)

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